

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/914,006C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial *anything*, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or contains Artificial.

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response contains the word "Artificial" or "Unknown." Please explain source of genetic material in <220> to <223> section, i.e., why you chose Artificial or Unknown. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn
 "bug" Please do not use "Copy to Disk" function of PatentIn. In PatentIn 2.x it causes a corrupted file and in PatentIn 3.x you may lose your hard returns in the sequence listing. Instead, please use "Windows Explorer" or any other manual means to copy file to floppy disk.



PCT

RAW SEQUENCE LISTING

DATE: 01/22/2003

PATENT APPLICATION: US/09/914,006C

TIME: 13:42:48

Input Set : A:\SN09914006.asc

Output Set: N:\CRF4\01222003\I914006C.raw

3 <110> APPLICANT: Eggeling, Lothar
 4 Sahm, Hermann
 6 <120> TITLE OF INVENTION: METHOD FOR MICROBially PRODUCING L-VALINE
 8 <130> FILE REFERENCE: 5899*13
 10 <140> CURRENT APPLICATION NUMBER: 09/914006C
 C--> 11 <141> CURRENT FILING DATE: 2002-11-07
 13 <150> PRIOR APPLICATION NUMBER: PCT/EP00/01405
 14 <151> PRIOR FILING DATE: 2000-02-21
 16 <160> NUMBER OF SEQ ID NOS: 7
 18 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2952
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Corynebacterium glutamicum
 25 <400> SEQUENCE: 1

E--> 26 agtacttggga gcgcca~~aa~~ag gcactgggca agccagttca gttgaacttc
 27 gatgacgaca 60
 E--> 29 ccgatgggaa tacaacacaa acagaaagcg ttgaatccca agagaccgga
 30 caagccgcgt 120
 E--> 32 ctgaaacctc acatcgtgat aaccctgcgt cacagcacta gagtgtata
 33 agccgtccga 180
 E--> 35 accaaaggtc cacacctctg cagcagtaga agctcaccga agttttcaaa
 36 gtgccgttga 240
 E--> 38 ttcttgacaa ccacccgcgc ctcttttagag cagatttgaa aagcgcacga
 39 tgatcccact 300
 E--> 41 tcgttcaaaa gtcaccacgc tcggtgcgaa tgcagctggc gctcgcgcgc
 42 ttggcggtgc 360
 E--> 44 caccggcacc aaggaaatg agttcggcaa gccaatgtgt gccatcgtaa
 45 actcctacac 420
 E--> 47 ccagttcgtg ccgggacacg ttcaccttaa gaacgtcggc gatattgtgg
 48 cagatgcagt 480
 E--> 50 ggcgcaaagcc ggtggcggttc caaaggaatt caacaccatc gtogatgaog
 51 gcatcgccat 540
 E--> 53 gggacacggc ggcattgtgt actccctgcc atcccgtaga atcatcgccg
 54 actccgtcga 600
 E--> 56 ataatgggc aacgcacaca ccgcgcacgc catggtgtgt atctccaaact
 57 gtgacaagat 660
 E--> 59 caecccaggc atgctcaacg cagcaatgcg cctgaacatc ccagtggtct
 60 tcgtttccgg 720

move wrapped sequences &
 numbering back to previous
 line, See item #1
 on ERROR Summary
 SHEET and 37CFR
 1.822 (e)

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DATE: 01/22/2003

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Input Set : A:\SN09914006.asc

Output Set: N:\CRF4\01222003\I914006C.raw

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E--> 62 tgcccaatg gaagctggca aggtgtcgt cgttgagcgc gttgcacacg
63 caccaaccga 780
E--> 65 cctcatcacc gcgatctccg catccgcaag cgatgcagtc gacgacgcag
66 gccttgacgc 840
E--> 68 cgttgaacga tccgcatgcc caacctgtgg ctctgtctcc ggtatgttca
69 ccgcgaactc 900
E--> 71 catgaactgc ctccacgaag ctctgggact ttctctcccg ggcaacggct
72 ccactctggc 960
E--> 74 aacccacgcga gcacgtcgcg cactgtttga aaaggccggc gaaaccgtcg
75 ttgaactgtg 1020
E--> 77 ccgcgcgtac tacggtgaag aagacgaatc cgtttctgcca cgtggcattg
78 ccaccaagaa 1080
E--> 80 ggcattcgaa aacgcaatgg cactggatat ggccatgggt ggatccacca
81 acaccatcct 1140
E--> 83 ccacatcctc gcagctgccc aggaaggcga agttgacttc gacctcgcag
84 acatcgacga 1200
E--> 86 actgtccaaa aacgtcccct gcctgtccaa ggttgacca aactccgact
87 accacatgga 1260
E--> 89 agacgtccac cgcgcgggtc gcattccagc actgctcggc gagctcaacc
90 gcggtggcct 1320
E--> 92 gctgaacaag gacgtccact ccgttcactc caacgacctt gaagggttgg
93 tggatgactg 1380
E--> 95 ggatatccgc tctggcaaga ccaccgaagt agcaaccgaa ctcttccacg
96 cagccccagg 1440
E--> 98 tggcatccgc accaccgaag cattctccac cgagaaccgc tgggacgaac
99 tgcacaccga 1500
E--> 101 cgctgccaag ggctgcatcc gcgacgttga acacgcctac accgccgacg
102 gcggcctggt 1560
E--> 104 tgttcttcgc ggcaacatct cccctgacgg cgcagtgatc aagtccgcag
105 gtatcgaaga 1620
E--> 107 agagctgtgg aacttcaccg gaccagcacg agttgtcgaa agccaggaag
108 aggcagtctc 1680
E--> 110 tgtcatcctg accaagacca tccaagctgg cgaagttctg gtcgtccgct
111 acgaaggccc 1740
E--> 113 atcagggtgga ccaggcatgc aggaaatgct tcacccaacc gcattcctca
114 agggatccgg 1800
E--> 116 cctgggcaag aagtgtgcac tgatcacoga cggccgtttc tccggagggt
117 cctcaggact 1860
E--> 119 gtccatcggc cacgtctccc cagaagcagc acacggcgga gtcattggtc
120 tgatcgaaaa 1920
E--> 122 cggcgacatc gtctccatcg acgttcacaa ccgcaagctc gaagttcagg
123 tctccgacga 1980
E--> 125 ggaactccag cgcgcgcgcg acgttatgaa cgcctccgag aagccatggc
126 agccagtcaa 2040
E--> 128 cgttaaccgc gttgtcacca aggcaactgc gcataacgca aagatggcta
129 cctccgctga 2100
E--> 131 taagggtgca gtccgtcagg tcgactaacc ctttgtgagt gtttgagcac
132 cgttcccta 2160
E--> 134 ctttgggttc cgggtcttt tcatgtcttg gcctgtgtgg gcgtgggtga

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Same as page 1

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Input Set : A:\SN09914006.asc

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135 gctccccgtt 2220
E--> 137 gcaaatactc accacaagt gcaggatttc tgctggttgt ggtggatttt
138 cccgctttat 2280
E--> 140 agccctatgc gtgcaacttt cggaccgatt ccaaagggca aagccctgtt
141 tgtggtggat 2340
E--> 143 ccttgccctg gaagctttca ggaaccacaa ctaccccaact gaccccaaag
144 tggataggcc 2400
E--> 146 ctattcttcc gtttaagcgc ctcaaaccac tctccccaca cttgacccat
147 taggcaatta 2460
E--> 149 cgaatcctta aacagccttc tacagcacca tgccccaac cgaaccagg
150 catgaaaaag 2520
E--> 152 accctcacca ggagggtctt tttctaaaac tttggctacg cgattggggt
153 cacaccgca 2580
E--> 155 ccgaaccacc acagcagaac tgccgctgcg atgccgatga ccacgaagat
156 ccacgagctc 2640
E--> 158 accagtggac gctttgcca acctcggcca gagtcaaggg aaatcttgcc
159 ggggccgggtg 2700
E--> 161 aactgaagtc cgacaaccac gatagtgagg atcagtgcc gcatcaatgg
162 ctactaagt 2760
E--> 164 tcacccaac caccttcac agtggtgact tgggtgaaggg tggtaaagga
165 tgtcgccacc 2820
E--> 167 gtggctaccg ctgctgccac tggggtcac agaccaagga gcaggaagac
168 accagccgca 2880
E--> 170 agttcaatag atggaagcag gatcgcgagg atttcaggcc actggtaacc
171 agcgaactct 2940
E--> 173 gcctcgactc ta
174 2952
177 <210> SEQ ID NO: 2
178 <211> LENGTH: 612
179 <212> TYPE: PRT
180 <213> ORGANISM: Corynebacterium glutamicum
182 <400> SEQUENCE: 2
184 Met Ile Pro Leu Arg Ser Lys Val Thr Thr Val Gly Arg Asn Ala
E--> 185 Ala
E--> 186 1 5 10 15
189 Gly Ala Arg Ala Leu Trp Arg Ala Thr Gly Thr Lys Glu Asn Glu
E--> 190 Phe
E--> 191 20 25 30
194 Gly Lys Pro Ile Val Ala Ile Val Asn Ser Tyr Thr Gln Phe Val
E--> 195 Pro
E--> 196 35 40 45
199 Gly His Val His Leu Lys Asn Val Gly Asp Ile Val Ala Asp Ala
E--> 200 Val
E--> 201 50 55 60
204 Arg Lys Ala Gly Gly Val Pro Lys Glu Phe Asn Thr Ile Val Asp
E--> 205 Asp
E--> 206 65 70 75 80
209 Gly Ile Ala Met Gly His Gly Gly Met Leu Tyr Ser Leu Pro Ser
E--> 210 Arg

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Same as page 1

Same as page 1

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/914,006C

DATE: 01/22/2003

TIME: 13:42:48

Input Set : A:\SN09914006.asc

Output Set: N:\CRF4\01222003\I914006C.raw

Same as page 1

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E--> 211      85      90      95
      214 Glu Ile Ile Ala Asp Ser Val Glu Tyr Met Val Asn Ala His Thr
E--> 215 Ala
E--> 216      100      105      110
      219 Asp Ala Met Val Cys Ile Ser Asn Cys Asp Lys Ile Thr Pro Gly
E--> 220 Met
E--> 221      115      120      125
      224 Leu Asn Ala Ala Met Arg Leu Asn Ile Pro Val Val Phe Val Ser
E--> 225 Gly
E--> 226      130      135      140
      229 Gly Pro Met Glu Ala Gly Lys Ala Val Val Val Glu Arg Val Ala
E--> 230 His
E--> 231      145      150      155
E--> 232      160
      235 Ala Pro Thr Asp Leu Ile Thr Ala Ile Ser Ala Ser Ala Ser Asp
E--> 236 Ala
E--> 237      165      170      175
      240 Val Asp Asp Ala Gly Leu Ala Ala Val Glu Arg Ser Ala Cys Pro
E--> 241 Thr
E--> 242      180      185      190
      245 Cys Gly Ser Cys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Cys
E--> 246 Leu
E--> 247      195      200      205
      250 Thr Glu Ala Leu Gly Leu Ser Leu Pro Gly Asn Gly Ser Thr Leu
E--> 251 Ala
E--> 252      210      215      220
      255 Thr His Ala Ala Arg Arg Ala Leu Phe Glu Lys Ala Gly Glu Thr
E--> 256 Val
E--> 257      225      230      235
E--> 258      240
      261 Val Glu Leu Cys Arg Arg Tyr Tyr Gly Glu Glu Asp Glu Ser Val
E--> 262 Leu
E--> 263      245      250      255
      266 Pro Arg Gly Ile Ala Thr Lys Lys Ala Phe Glu Asn Ala Met Ala
E--> 267 Leu
E--> 268      260      265      270
      271 Asp Met Ala Met Gly Gly Ser Thr Asn Thr Ile Leu His Ile Leu
E--> 272 Ala
E--> 273      275      280      285
      276 Ala Ala Gln Glu Gly Glu Val Asp Phe Asp Leu Ala Asp Ile Asp
E--> 277 Glu
E--> 278      290      295      300
      281 Leu Ser Lys Asn Val Pro Cys Leu Ser Lys Val Ala Pro Asn Ser
E--> 282 Asp
E--> 283      305      310      315
E--> 284      320
      287 Tyr His Met Glu Asp Val His Arg Ala Gly Arg Ile Pro Ala Leu
E--> 288 Leu
E--> 289      325      330      335

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Input Set : A:\SN09914006.asc

Output Set: N:\CRF4\01222003\I914006C.raw

292 Gly Glu Leu Asn Arg Gly Gly Leu Leu Asn Lys Asp Val His Ser
 E--> 293 Val
 E--> 294 340 345 350
 297 His Ser Asn Asp Leu Glu Gly Trp Leu Asp Asp Trp Asp Ile Arg
 E--> 298 Ser
 E--> 299 355 360 365
 302 Gly Lys Thr Thr Glu Val Ala Thr Glu Leu Phe His Ala Ala Pro
 E--> 303 Gly
 E--> 304 370 375 380
 307 Gly Ile Arg Thr Thr Glu Ala Phe Ser Thr Glu Asn Arg Trp Asp
 E--> 308 Glu
 E--> 309 385 390 395
 E--> 310 400
 313 Leu Asp Thr Asp Ala Ala Lys Gly Cys Ile Arg Asp Val Glu His
 E--> 314 Ala
 E--> 315 405 410 415
 318 Tyr Thr Ala Asp Gly Gly Leu Val Val Leu Arg Gly Asn Ile Ser
 E--> 319 Pro
 E--> 320 420 425 430
 323 Asp Gly Ala Val Ile Lys Ser Ala Gly Ile Glu Glu Glu Leu Trp
 E--> 324 Asn
 E--> 325 435 440 445
 328 Phe Thr Gly Pro Ala Arg Val Val Glu Ser Gln Glu Glu Ala Val
 E--> 329 Ser
 E--> 330 450 455 460
 333 Val Ile Leu Thr Lys Thr Ile Gln Ala Gly Glu Val Leu Val Val
 E--> 334 Arg
 E--> 335 465 470 475
 E--> 336 480
 339 Tyr Glu Gly Pro Ser Gly Gly Pro Gly Met Gln Glu Met Leu His
 E--> 340 Pro
 E--> 341 485 490 495
 344 Thr Ala Phe Leu Lys Gly Ser Gly Leu Gly Lys Lys Cys Ala Leu
 E--> 345 Ile
 E--> 346 500 505 510
 349 Thr Asp Gly Arg Phe Ser Gly Gly Ser Ser Gly Leu Ser Ile Gly
 E--> 350 His
 E--> 351 515 520 525
 354 Val Ser Pro Glu Ala Ala His Gly Gly Val Ile Gly Leu Ile Glu
 E--> 355 Asn
 E--> 356 530 535 540
 359 Gly Asp Ile Val Ser Ile Asp Val His Asn Arg Lys Leu Glu Val
 E--> 360 Gln
 E--> 361 545 550 555
 E--> 362 560
 365 Val Ser Asp Glu Glu Leu Gln Arg Arg Arg Asp Ala Met Asn Ala
 E--> 366 Ser
 E--> 367 565 570 575
 370 Glu Lys Pro Trp Gln Pro Val Asn Arg Asn Arg Val Val Thr Lys

Same as page 1

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TIME: 13:42:48

Input Set : A:\SN09914006.asc

Output Set: N:\CRF4\01222003\I914006C.raw

E--> 371 *Ala* *Same as page 1*
 E--> 372 580 585 590
 375 Leu Arg Ala Tyr Ala Lys Met Ala Thr Ser Ala Asp Lys Gly Ala
 E--> 376 *Val*
 E--> 377 595 600 605
 380 Arg Gln Val Asp
 E--> 381 610
 384 <210> SEQ ID NO: 3
 385 <211> LENGTH: 2164
 386 <212> TYPE: DNA
 387 <213> ORGANISM: Corynebacterium glutamicum
 389 <400> SEQUENCE: 3
 E--> 390 *gcttcgggg* accaattcct ttaagaacca tcagatcaat ctgtttgtaca
 391 ttctcggcca 60
 E--> 393 gattcagctt ttcggtaagg acgaaacact ttcacttgaa tcggcagcaa
 394 agtttcttaa 120
 E--> 396 agtttctaag gcaactgcaa cgaggatatt tagaactctc cgagaaatgg
 397 aattagttca 180
 E--> 399 cgaggtcagc aaacgccctt tgcggtttgc gctcacggat aaaggctcgtg
 400 agatagtagg 240
 E--> 402 *tcttgaggta* *Same as page 1* aaaatttgac tcataacga gaacttaatc gagcaacacc
 403 cctgaacagt 300
 E--> 405 gaatcaaatac ggaatttatt tattctgagc tggatcatcac atctatactc
 406 atgcccattgt 360
 E--> 408 caggcatttga tgcaaaagaaa atccgcaccc gtcatttcog cgaagctaaa
 409 gtaaacggcc 420
 E--> 411 agaaaagtttc ggttctcacc agctatgatg cgctttcggc gcgcattttt
 412 gatgaggctg 480
 E--> 414 gcgtcgatat gctccttggt ggtgattcog ctgccaacgt tgtgctgggt
 415 cgcgatacca 540
 E--> 417 ccttgtcgat caccttggtat gagatgattg tgctggccaa ggcggtgacg
 418 atcgctacga 600
 E--> 420 agcgtgcgct tgtggtggtt gatctgcogt ttggtacctt tgagggtgagc
 421 ccaaatcagg 660
 E--> 423 cgggtggagtc cgcgatccgg gtcattcgtg aaacgggtgc ggctgcgggtg
 424 aagatcgagg 720
 E--> 426 gtggcgtgga gatcgcgag acgattcgac gcattgttga tgctggaatt
 427 ccggttgctg 780
 E--> 429 gccacatcgg gtacaccccg cagtcogagc attccttggg cggccacgtg
 430 gttcagggtc 840
 E--> 432 gtggcgcgag ttctggaaag ctcatcgccg atgccgcgcg gttggagcag
 433 gcgggtgcgt 900
 E--> 435 ttgcggttgt gttggagatg gttocagcag aggcagcgcg cgaggttacc
 436 gaggatcttt 960
 E--> 438 ccatcaccac tatcggaatc ggtgcocggca atggcacaga tgggcagggt
 439 ttggtgtggc 1020
 E--> 441 aggatgcctt cggcctcaac cgcggcaaga agccacgctt cgtccgcgag
 442 tacgccacct 1080
 E--> 444 tgggcgattc cttgcacgac gcgcgcgagg cctacatcgc cgatatccac

RAW SEQUENCE LISTING

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TIME: 13:42:48

Input Set : A:\SN09914006.asc

Output Set: N:\CRF4\01222003\I914006C.raw

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445 gcgggtacct 1140
E--> 447 tcccaggcga agcggagtcc ttttaatgca ggtagcaacc acaaagcagg
448 cgcttatcga 1200
E--> 450 cgcctcctc caccacaaat cgcggtgggt cgtccccacc atgggtgcgc
451 tacacagcgg 1260
E--> 453 acacgcctcg ttggttaaag cagcacgcgc tgaaaacgac actggtgtag
454 ccagtatttt 1320
E--> 456 tgtcaatccc ctgcagtttg aagcactcgg tgattgcgat gattaccgca
457 actatccccg 1380
E--> 459 ccaactcgac gccgatttag cactgcttga agaggcaggt gtggatattg
460 tgttcgacc 1440
E--> 462 cgatgtggag gaaatgtacc cgggtggctt gccactagtg tgggcgcgca
463 ccggttccat 1500
E--> 465 cggaacaaaa ttggagggtg ccagcaggcc tggccatttc gatggtgtgg
466 ctaccgtggt 1560
E--> 468 ggcgaaactg ttcaatttgg tgcgcctga tegtgcata tttggacaaa
469 aagatgctca 1620
E--> 471 gcaggttgcg gtgattcggc gattggttgc cgatctagac attcccgtag
472 agattcgctc 1680
E--> 474 cgttcgatt attcgtggcg ccgatggctt agccgaatcc agccgcaatc
475 aacgtctttc 1740
E--> 477 tgcggatcag cgagcgcaag ctctgggtgt gccgcaggtg ttgagtgggt
478 tgcagcgtcg 1800
E--> 480 aaaagcagct ggtgaagcgc tagatatcca aggtgcgcgc gacaccttgg
481 ccagcgccga 1860
E--> 483 cggcgtgcgc ttggatcacc tggaaattgt cgatccagcc accctcgaac
484 cattagaaat 1920
E--> 486 cgacggcctg ctacccaac cagcgttggt ggtcggcgcg attttcgtgg
487 ggccggtgcg 1980
E--> 489 gttgatcgac aatatcgagc tctagtacca accctgcggt gcagcacgca
490 gcttcgcata 2040
E--> 492 acgcgtgctc agctcagtgt ttttaggtgc gcggtgcgga toggaaccgg
493 gagttggcca 2100
E--> 495 ctgcggtggc gtggcctcac ccgacagcgc ccattgcgcg tgacgagctg
496 caccacacgc 2160
E--> 498 caca
499 2164
502 <210> SEQ ID NO: 4
503 <211> LENGTH: 271
504 <212> TYPE: PRT
505 <213> ORGANISM: Corynebacterium glutamicum
507 <400> SEQUENCE: 4
509 Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His
E--> 510 Phe
E--> 511 1 5 10 15
514 Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser
E--> 515 Tyr
E--> 516 20 25 30
519 Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met

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*Same as page 1**Same as page 1*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/914,006C

DATE: 01/22/2003

TIME: 13:42:48

Input Set : A:\SN09914006.asc

Output Set: N:\CRF4\01222003\I914006C.raw

E--> 520 Leu
 E--> 521 35 40 45
 524 Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr
 E--> 525 Thr
 E--> 526 50 55 60
 529 Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val
 E--> 530 Thr
 E--> 531 65 70 75 80
 534 Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly
 E--> 535 Thr
 E--> 536 85 90 95
 539 Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val
 E--> 540 Met
 E--> 541 100 105 110
 544 Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu
 E--> 545 Ile
 E--> 546 115 120 125
 549 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val
 E--> 550 Gly
 E--> 551 130 135 140
 554 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His
 E--> 555 Val
 E--> 556 145 150 155
 E--> 557 160
 560 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala
 E--> 561 Arg
 E--> 562 165 170 175
 565 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val
 E--> 566 Pro
 E--> 567 180 185 190
 570 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr
 E--> 571 Ile
 E--> 572 195 200 205
 575 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp
 E--> 576 Gln
 E--> 577 210 215 220
 580 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg
 E--> 581 Glu
 E--> 582 225 230 235
 E--> 583 240
 586 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr
 E--> 587 Ile
 E--> 588 245 250 255
 591 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 E--> 592 260 265 270
 595 <210> SEQ ID NO: 5
 596 <211> LENGTH: 279
 597 <212> TYPE: PRT
 598 <213> ORGANISM: Corynebacterium glutamicum

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Input Set : A:\SN09914006.asc

Output Set: N:\CRF4\01222003\I914006C.raw

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600 <400> SEQUENCE: 5
602 Met Gln Val Ala Thr Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu
E--> 603 His
E--> 604 1 Same as page 1 5 10 15
607 His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser
E--> 608 Gly
E--> 609 20 25 30
612 His Ala Ser Leu Val Lys Ala Ala Arg Ala Glu Asn Asp Thr Val
E--> 613 Val
E--> 614 35 40 45
617 Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp
E--> 618 Cys
E--> 619 50 55 60
622 Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala
E--> 623 Leu
E--> 624 65 70 75 80
627 Leu Glu Glu Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Glu
E--> 628 Glu
E--> 629 85 90 95
632 Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser
E--> 633 Ile
E--> 634 100 105 110
637 Gly Thr Lys Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp Gly
E--> 638 Val
E--> 639 115 120 125
642 Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg
E--> 643 Ala
E--> 644 130 135 140
647 Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg
E--> 648 Leu
E--> 649 145 150 155
E--> 650 160
653 Val Ala Asp Leu Asp Ile Pro Val Glu Ile Arg Pro Val Pro Ile
E--> 654 Ile
E--> 655 165 170 175
658 Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu
E--> 659 Ser
E--> 660 180 185 190
663 Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser
E--> 664 Gly
E--> 665 195 200 205
668 Leu Gln Arg Arg Lys Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly
E--> 669 Ala
E--> 670 210 215 220
673 Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu
E--> 674 Glu
E--> 675 225 230 235
E--> 676 240
679 Ile Val Asp Pro Ala Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/914,006C

DATE: 01/22/2003

TIME: 13:42:48

Input Set : A:\SN09914006.asc

Output Set: N:\CRF4\01222003\I914006C.raw

E--> 680 Leu *Same as page 1*
E--> 681 245 250 255
684 Thr Gln Pro Ala Leu Val Val Gly Ala Ile Phe Val Gly Pro Val
E--> 685 Arg
E--> 686 260 265 270
689 Leu Ile Asp Asn Ile Glu Leu
E--> 690 275
693 <210> SEQ ID NO: 6
694 <211> LENGTH: 26
695 <212> TYPE: DNA
696 <213> ORGANISM: Corynebacterium glutamicum
698 <400> SEQUENCE: 6
E--> 699 gagaacttaa tcgagcaaca cccctg
700 26
703 <210> SEQ ID NO: 7
704 <211> LENGTH: 26
705 <212> TYPE: DNA
706 <213> ORGANISM: Corynebacterium glutamicum
708 <400> SEQUENCE: 7
E--> 709 gcgccacgcc tagccttggc cctcaa
710 26

VERIFICATION SUMMARY

DATE: 01/22/2003

PATENT APPLICATION: US/09/914,006C

TIME: 13:42:49

Input Set : A:\SN09914006.asc

Output Set: N:\CRF4\01222003\I914006C.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1
M:254 Repeated in SeqNo=1
L:185 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:390 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:3
M:254 Repeated in SeqNo=3
L:510 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:603 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:699 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:6
L:709 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:7